

## SEQUENCE LISTING

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ggg gag Gly Glu	g ctg I Leu	tgg Trp 20	Pro	gga Gly	Ala	Glu	Ala	Arg	gca Ala	gcg Ala	cct Pro	tac Tyr 30	999 Gly	gtc Val	96
agg ctt Arg Leu	tgc Cys 35	ggc Gly	cga Arg	gaa Glu	ttc Phe	atc Ile 40	cga Arg	gca Ala	gtc Val	atc Ile	ttc Phe 45	acc Thr	tgc Cys	999 Gly	144
ggc tcc Gly Ser 50	Arg	tgg Trp	aga Arg	cga Arg	tca Ser 55	gac Asp	atc Ile	ctg Leu	gcc Ala	cac His 60	gag Glu	gct Ala	atg Met	gga Gly	192

gat Asp 65	) In	c tt r Ph	c cc e Pr	g ga o As	t gc p Al	a Ası	t gc o Ala	t ga a As <sub>l</sub>	t ga p G1	a ga u As 7	p Se	ıt ct er Le	g go u Al	a g a G	igc ily	gag Glu 80	240
ctg Leu	ga Asp	t ga o G1	g gc u Al	c ate a Me 8!	t Gly	g too / Ser	ago Ser	gaq Glu	g tg u Tr <sub>l</sub> 90	o Le	g gc u Al	c ct a Le	g ac u Th	r L	ag ys 95	tca Ser	288
ccc Pro	caç G1r	g gc	c tt a Ph 10	t tad e Tyn O	c agg r Arg	9 999 9 Gly	g oga V Arg	cco Pro 105	) Ser	c tgg r Trļ	g ca o Gl	a gga n Gly	a ac y Th 11	r P	ct ro	999 Gly	336
gtt Val	ctt Leu	cgg Arg 115	g GI	c ago y Ser	cga Arg	gat Asp	gto Val 120	Leu	get IAla	ggd Gly	c ct <sup>.</sup> / Lei	t tcd u Ser 125	^ Sei	c ag	gc er	tgc Cys	384
tgc Cys	aag Lys 130	Irp	9 999 9 Gly	g tgt ⁄Cys	agc Ser	aaa Lys 135	agt Ser	gaa Glu	ato Ile	: agt : Ser	ago Ser 140	Leu	tgo LCys	c ta			429
<210 <211 <212 <213	l> 1 2> P	42 RT	sapi	ens													
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1				Met 5					10					15			
Gly			20					25					30	G1	y \		
Arg	Leu	Cys 35	Gly	Arg	Glu	Phe	Ile 40	Arg	Ala	Val	Ile	Phe 45	Thr	Cy.	s (	Gly	
Gly	Ser 50		Trp	Arg	Arg	Ser 55		Ile	Leu	Ala		G]u	Ala	Me	t (	Sly	
Asp 65		Phe	Pro	Asp	A1a 70		Ala	Asp	Glu		60 Ser	Leu	Ala	G1 <sub>y</sub>			
Leu /	Asp	G1u	Ala	Met 85		Ser	Ser	G1u	Trp	75 Leu	Ala	Leu	Thr		5 S	30 Ser	
Pro (	Gln	Ala	Phe 100		Arg	Gly	Arg		90 Ser	Trp	G1n	G1y	Thr 110	95 Pro	G	ily	

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 Cys Lys Trp Gly Cys Ser Lys Ser Glu Ile Ser Ser Leu Cys
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<223> Each Xaa is independently any amino acid residue
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                                     10
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10
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Arg Xaa Xaa Xaa Arg
<210> 6
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<223> Degenerate polynucleotide sequence encoding the
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<221> variation
<222> (1)...(426)
<223> Each N is independently A, T, G, or C.
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                                                                    60
conggngong argonmgngo ngoncontay ggngtnmgny tntgyggnmg ngarttyath
                                                                   120
mgngcngtna thttyacntg yggnggnwsn mgntggmgnm gnwsngayat hytngcncay
                                                                   180
gargenatgg gngayaentt yeengaygen gaygengayg argaywsnyt ngenggngar
                                                                   240
ytngaygarg cnatgggnws nwsngartgg ytngcnytna cnaarwsncc ncargcntty
                                                                   300
taymgnggnm gnccnwsntg gcarggnacn ccnggngtny tnmgnggnws nmgngaygtn
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ytngcnggny tnwsnwsnws ntgytgyaar tggggntgyw snaarwsnga rathwsnwsn ytntgy	420 426
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<220> <223> Exon 1 antisense oligonucleotide primer	

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<211> 41
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<213> Artificial Sequence
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<213> Artificial Sequence
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<223> Exon 2 antisense oligonucleotide primer
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                                                                         52
<210> 13
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<222> (1)...(4)
<223> Xaa = Any Amino Acid
<400> 13
Arg Xaa Xaa Arg
1
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